

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/494,585

DATE: 08/15/2001  
TIME: 12:29:51

Input Set : A:\Cura57U1.APP  
Output Set: N:\CRF3\08152001\I494585.raw

# ENTERED

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3 <110> APPLICANT: Shimkets, Richard A
4   Prayaga, Sudhirdas K
6 <120> TITLE OF INVENTION: Novel Fibroblast Growth Factor and Nucleic Acids
7   Encoding Same
9 <130> FILE REFERENCE: 15966-557 FGF-CX
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/494,585
C--> 12 <141> CURRENT FILING DATE: 2001-01-31
14 <150> PRIOR APPLICATION NUMBER: USSN 60/145,899
15 <151> PRIOR FILING DATE: 1999-07-27
17 <160> NUMBER OF SEQ ID NOS: 13
19 <170> SOFTWARE: PatentIn Ver. 2.1
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22 <211> LENGTH: 633
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(633)
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33   1           5           10           15
35 ttg ggc cag cag gtg ggt tcg cat ttc ctg ttg cct cct gcc ggg gag 96
36 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu
37           20           25           30
39 cgg ccg ccg ctg ctg ggc gag cgc agg agc gcg gcg gag cgg agc gcg 144
40 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala
41           35           40           45
43 cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc atc ctg 192
44 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
45           50           55           60
47 cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg 240
48 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
49   65           70           75           80
51 ccc gac ggc agc gtg cag ggc acc cgg cag gac cac agc ctc ttc ggt 288
52 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
53           85           90           95
55 atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt 336
56 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
57           100          105          110
59 gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat 384
60 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
61           115          120          125
63 gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa 432
64 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
65           130          135          140
67 gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac 480

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68 Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
69 145 150 155 160
71 act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga 528
72 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
73 165 170 175
75 gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct 576
76 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
77 180 185 190
79 aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag gac cta ctg 624
80 Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu
81 195 200 205
83 atg tac act 633
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90 <212> TYPE: PRT
91 <213> ORGANISM: Homo sapiens
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97 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu
98 20 25 30
100 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala
101 35 40 45
103 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
104 50 55 60
106 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
107 65 70 75 80
109 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
110 85 90 95
112 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
113 100 105 110
115 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
116 115 120 125
118 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
119 130 135 140
121 Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
122 145 150 155 160
124 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
125 165 170 175
127 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
128 180 185 190
130 Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu
131 195 200 205
133 Met Tyr Thr
134 210
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 38

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140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
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153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
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163 <211> LENGTH: 424
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169 tagaaatctt cccaatggt actatccagg gaaccaggaa agaccacagc cgatttggca 120
170 ttctggaatt tatcagtata gcagtgggcc tggtcagcat tcgaggcgtg gacagtggac 180
171 tctacctcgg gatgaatgag aagggggagc tgtatggatc agaaaaacta acccaagagt 240
172 gtgtattcag agaacagttc gaagaaaact ggtataatac gtactcgtca aacctatata 300
173 agcacgtgga cactggaagg cgatactatg ttgcattaaa taaagatggg accccgagag 360
174 aagggaactag gactaaacgg caccagaaat tcacacattt tttacctaga ccagtggacc 420
175 ccga 424
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185 ggtggaagcc ggtgcggcaa tagagctgcc ggcgcgcagg atgccgtgca ggtgcgccag 120
186 ctgcgcagcc cccggcccgc cgcgcgcgct ccgctccgcc gcgctcctgc gctcgcccag 180
187 cagcggcggc cgctccccgg caggaggcaa caggaaatgc gaaccacct gctggcccaa 240
188 gccctccagg ccgcccagaa agcccccgac ttcggctaag ggagccat 288
191 <210> SEQ ID NO: 7
192 <211> LENGTH: 255
193 <212> TYPE: DNA
194 <213> ORGANISM: Homo sapiens
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198 taagaaatgt gtaaatttct gatgcctctt ggacctggcg ccatctcttg gagttccgtc 120
199 tttgttaagt gccacaaaat acctgcggcc agtgtctcca tgtttatata tgtagatga 180
200 ataggtgtta taccagttct cttcaaactg ctccctaaag atgcattcgg aagtaagttt 240
201 ctccctgaaag agaga 255
204 <210> SEQ ID NO: 8
205 <211> LENGTH: 106

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206 <212> TYPE: DNA
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209 <400> SEQUENCE: 8
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217 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 9
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224 20 25 30
226 Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
227 35 40 45
229 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
230 50 55 60
232 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
233 65 70 75 80
235 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
236 85 90 95
238 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
239 100 105 110
241 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
242 115 120 125
244 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
245 130 135 140
247 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
248 145 150 155 160
250 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
251 165 170 175
253 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
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256 Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser
257 195 200 205
263 <210> SEQ ID NO: 10
264 <211> LENGTH: 208
265 <212> TYPE: PRT
266 <213> ORGANISM: Mus sp.
268 <400> SEQUENCE: 10
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270 1 5 10 15
272 Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
273 20 25 30
275 Leu Asn Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
276 35 40 45
278 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
279 50 55 60

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281 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
282 65 70 75 80
284 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
285 85 90 95
287 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
288 100 105 110
290 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
291 115 120 125
293 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
294 130 135 140
296 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
297 145 150 155 160
299 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
300 165 170 175
302 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
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305 Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser
306 195 200 205
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313 <211> LENGTH: 208
314 <212> TYPE: PRT
315 <213> ORGANISM: Rattus sp.
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321 Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
322 20 25 30
324 Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
325 35 40 45
327 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
328 50 55 60
330 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
331 65 70 75 80
333 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
334 85 90 95
336 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
337 100 105 110
339 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
340 115 120 125
342 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
343 130 135 140
345 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
346 145 150 155 160
348 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
349 165 170 175
351 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
352 180 185 190
354 Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser
355 195 200 205

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## VERIFICATION SUMMARY

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Input Set : A:\Cura57U1.APP

Output Set: N:\CRF3\08152001\I494585.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date